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SEQUENCE LISTING

TECH CENTER 1600/2900

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(1) GENERAL INFORMATION

- (i) APPLICANT: Coughlin, Shaun R.
Ishihari, Hiroaki
Connolly, Andrew
- (ii) TITLE OF THE INVENTION: Protease-Activated Receptor
3 and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/208,629
(B) FILING DATE: 08-DEC-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/742,440
(B) FILING DATE: 30-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Catherine M. Polizzi
(B) REGISTRATION NUMBER: 40,130
(C) REFERENCE/DOCKET NUMBER: 220002060310
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 813-5600
(B) TELEFAX: (650) 494-0792
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|------|
| TGACTTTGTA | TACTTAACAA | CATCCTGTAG | CCGGGTCTCA | GGACATCAAG | ATGAAAATCC | 60 |
| TTATCTTGGT | TGCAGCTGGG | CTGCTGTTTC | TGCCAGTCAC | TGTTTGCCAA | AGTGGCATAA | 120 |
| ATGTTTCAGA | CAACTCAGCA | AAGCCAACCT | TAACATTAA | GAGTTTAAAT | GGGGGTCCCC | 180 |
| AAAATACCTT | TGAAGAATTC | CCACTTTCTG | ACATAGAGGG | CTGGACAGGA | GCCACCACAA | 240 |
| CTATAAAAGC | GGAGTGTCCC | GAGGACAGTA | TTTCAACTCT | CCACGTGAAT | AATGCTACCA | 300 |
| TAGGATACCT | GAGAAGTTCC | TTAAGTACCC | AAGTGATACC | TGCCATCTAT | ATCCTGCTGT | 360 |
| TTGTGGTTGG | TGTACCATCC | AACATCGTGA | CCCTGTGGAA | ACTCTCCTTA | AGGACCAAAT | 420 |
| CCATCAGTCT | GGTCATCTTT | CACACCAACC | TGGCCATCGC | AGATCTCCTT | TTCTGTGTCA | 480 |
| CACTGCCATT | TAAGATCGCC | TACCATCTCA | ATGGCAACAA | CTGGGTATTT | GGCGAGGTCA | 540 |
| TGTGCCGGAT | CACCACGGTC | GTTTTCTACG | GCAACATGTA | CTGCGCTATC | CTGATCCTCA | 600 |
| CTTGTCATGGG | CATCAACCGC | TACCTGGCCA | CGGCTCACCC | TTTCACATAC | CAGAAGCTGC | 660 |
| CCAAACGCAG | CTTCTCCTTG | CTCATGTGTG | GCATAGTGTG | GGTCATGGTT | TTCTTATACA | 720 |
| TGCTGCCCTT | TGTCATCCTG | AAGCAGGAGT | ACCACCTCGT | CCACTCAGAG | ATCACCACCT | 780 |
| GCCACGATGT | CGTCGACGCG | TGCGAGTCCC | CATCATCCTT | CCGATTCTAC | TACTTCGTCT | 840 |
| CCTTAGCATT | CTTTGGGTTC | CTCATCCCCT | TTGTGATCAT | CATCTTCTGT | TACACGACTC | 900 |
| TCATCCACAA | ACTTAAATCA | AAGGATCGGA | TATGGCTGGG | CTACATCAAG | GCCGTCTCTC | 960 |
| TCATCCTTGT | GATTTTCACA | ATTTGCTTTG | CCCCACCAA | CATCATACTC | GTAATCCACC | 1020 |
| ATGCCAACTA | CTACTACCAC | AATACCGACA | GCTTGTAATT | TATGTATCTT | ATTGCTCTGT | 1080 |
| GCCTGGGGAG | CCTGAATAGC | TGCCTAGATC | CATTCTTTTA | CTTTGTCTATG | TCGAAAGTTG | 1140 |
| TAGATCAGCT | TAATCCTTAG | TCGGCAATGG | CAAGACCACT | TTAGAGACCA | AGGAGAGATA | 1200 |
| TCTGGGAAGA | CATACATGCT | TGGC | | | | 1224 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CCATATGCTA | ATATTTCTCT | TCAATTACAG | GCATAAATGT | TTCAGACAAC | TCAGCAAAGC | 60 |
| CAACCTTAAC | TATTAAGAGT | TTTAATGGGG | GTCCCCAAAA | TACCTTTGAA | GAATTCNNNN | 120 |
| NNNTACAAC | CTCCATGTGA | ATAATGCTAC | CATGGGATAC | CTGAGAAGTT | CCTTAAGTAC | 180 |
| CAAAGTGATA | CCTGCCATCT | ACATCCTGGT | GTTTGTGATT | GGTGTACCAG | CGAACATCGT | 240 |
| GACCCTGTGG | AAACTCTCCT | CAAGACCAA | ATCCATCTGT | CTGGTCATCT | TTACACCAA | 300 |
| CCTGGCCATC | GCGGATCTCC | TTTTCTGTGT | CACGCTGCCG | TTTAAGATCN | NCCTACCATC | 360 |
| TCAATGGCAA | CAACTGGGTA | TTTGGCGAGG | TCATGTGCCG | GATCACCACG | GTCGTTTTCT | 420 |
| ACGGCAACAT | GTAATGCGCT | ANNNTCCTGA | TCCTCACCTG | CATGGGCATC | AACCGCTACC | 480 |
| TGGCCACGGC | TCACCCTTTC | ACATACCAGA | AGCTGCCCAA | ACGCAGCTTC | TCCATGCTCA | 540 |
| TGTGTGGCAT | GGTGTGGGTC | ATGGTTTTCT | TATACATGCT | GCCCTTTGTC | ATCCNNNAAG | 600 |
| CAGGAGTACC | ACCTCGTCCA | CTCCGAGATC | ACCACCTGCC | ACGATGTCGT | CGACGCGTGC | 660 |
| GANTCCCCAT | CATCCTTCCG | ATTCTACTAC | TTCGTCTCCT | TAGCATTCTT | TGGGTTCCCTC | 720 |
| ATCCCGTTTG | TGATCATCAT | CTTCTGTTAC | ACGACTCTCA | TCCACAAACT | TAAATCAAAA | 780 |
| GATCNGATAT | GGCTGGGCTA | CATCAAGGCC | GTCCTCCTCA | TCCTTGTAAG | TTTCACCATC | 840 |
| TGCTTCCCCC | CCACCAAGNN | NNNNGATATC | TGGGAAGACG | TACATGCTTG | GCTGACTTGT | 900 |
| GCATGGCACC | ATCAGCTCAA | TTTTTAATTT | TTTAATTTTA | ATTTAATTTA | ATTTTATGTT | 960 |

| | |
|---|------|
| TTTGAGACAG AGCCTCACTG TGTAGTCCTG GCTGGCCTGG CTGGTTCTCT ATTTAGACCA | 1020 |
| GGTTAGCCTT GAACTCACAG AGATCTGCCT GCTTCTGCCT CCCAAGTGCT GGGTTCAACC | 1080 |
| AGGTCTGGCA AGCGCTCCAT TTTTCAGCTC CTCTGCAACA GTGC | 1124 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 5, 386, 394
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Tyr | Thr | Xaa | Gln | His | Pro | Val | Ala | Gly | Ser | Gln | Asp | Ile | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Met | Lys | Ile | Leu | Ile | Leu | Val | Ala | Ala | Gly | Leu | Leu | Phe | Leu | Pro | Val |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Thr | Val | Cys | Gln | Ser | Gly | Ile | Asn | Val | Ser | Asp | Asn | Ser | Ala | Lys | Pro |
| | 35 | | | | | 40 | | | | | | 45 | | | |
| Thr | Leu | Thr | Ile | Lys | Ser | Phe | Asn | Gly | Gly | Pro | Gln | Asn | Thr | Phe | Glu |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Glu | Phe | Pro | Leu | Ser | Asp | Ile | Glu | Gly | Trp | Thr | Gly | Ala | Thr | Thr | Thr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ile | Lys | Ala | Glu | Cys | Pro | Glu | Asp | Ser | Ile | Ser | Thr | Leu | His | Val | Asn |
| | | | 85 | | | | | | 90 | | | | 95 | | |
| Asn | Ala | Thr | Ile | Gly | Tyr | Leu | Arg | Ser | Ser | Leu | Ser | Thr | Gln | Val | Ile |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Pro | Ala | Ile | Tyr | Ile | Leu | Leu | Phe | Val | Val | Gly | Val | Pro | Ser | Asn | Ile |
| | | 115 | | | | | 120 | | | | | | 125 | | |
| Val | Thr | Leu | Trp | Lys | Leu | Ser | Leu | Arg | Thr | Lys | Ser | Ile | Ser | Leu | Val |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ile | Phe | His | Thr | Asn | Leu | Ala | Ile | Ala | Asp | Leu | Leu | Phe | Cys | Val | Thr |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | |
| Leu | Pro | Phe | Lys | Ile | Ala | Tyr | His | Leu | Asn | Gly | Asn | Asn | Trp | Val | Phe |
| | | | 165 | | | | | | 170 | | | | 175 | | |
| Gly | Glu | Val | Met | Cys | Arg | Ile | Thr | Thr | Val | Val | Phe | Tyr | Gly | Asn | Met |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Tyr | Cys | Ala | Ile | Leu | Ile | Leu | Thr | Cys | Met | Gly | Ile | Asn | Arg | Tyr | Leu |
| | 195 | | | | | | 200 | | | | | | 205 | | |
| Ala | Thr | Ala | His | Pro | Phe | Thr | Tyr | Gln | Lys | Leu | Pro | Lys | Arg | Ser | Phe |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ser | Leu | Leu | Met | Cys | Gly | Ile | Val | Trp | Val | Met | Val | Phe | Leu | Tyr | Met |
| 225 | | | | | 230 | | | | 235 | | | | | 240 | |
| Leu | Pro | Phe | Val | Ile | Leu | Lys | Gln | Glu | Tyr | His | Leu | Val | His | Ser | Glu |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Ile | Thr | Thr | Cys | His | Asp | Val | Val | Asp | Ala | Cys | Glu | Ser | Pro | Ser | Ser |
| | | 260 | | | | | | 265 | | | | | 270 | | |
| Phe | Arg | Phe | Tyr | Tyr | Phe | Val | Ser | Leu | Ala | Phe | Phe | Gly | Phe | Leu | Ile |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Pro | Phe | Val | Ile | Ile | Ile | Phe | Cys | Tyr | Thr | Thr | Leu | Ile | His | Lys | Leu |

| | | | | |
|---|---------------------|-----|--|-----|
| 290 | | 295 | | 300 |
| Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile | Lys Ala Val Leu Leu | | | |
| 305 | | 310 | | 320 |
| Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu | | | | |
| | | 325 | | 335 |
| Val Ile His His Ala Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr | | | | |
| | | 340 | | 350 |
| Phe Met Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu | | | | |
| | | 355 | | 365 |
| Asp Pro Phe Leu Tyr Phe Val Met Ser Lys Val Val Asp Gln Leu Asn | | | | |
| | | 370 | | 380 |
| Pro Xaa Ser Ala Met Ala Arg Pro Leu Xaa Arg Pro Arg Arg Asp Ile | | | | |
| | | 385 | | 400 |
| Trp Glu Asp Ile His Ala Trp | | | | |
| | | 405 | | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| TGCTCCATGA | TTTTACAGAT | TTCATAACGT | TTAAGAGACG | GGACTCAGGT | CATCAAAATG | 60 |
| AAAGCCCTCA | TCTTTGCAGC | TGCTGGCCTC | CTGCTTCTGT | TGCCCACCTT | TTGTCAGAGT | 120 |
| GGCATGGAAA | ATGATACAAA | CAACTTGGCA | AAGCCAACCT | TACCCATTAA | GACCTTTCGT | 180 |
| GGAGCTCCCC | CAAATTCTTT | TGAAGAGTTC | CCCTTTTCTG | CCTTGGAAGG | CTGGACAGGA | 240 |
| GCCACGATTA | CTGTAAAAAT | TAAGTGCCTT | GAAGAAAGTG | CTTCACATCT | CCATGTGAAA | 300 |
| AATGCTACCA | TGGGGTACCT | GACCAGCTCC | TTAAGTACTA | AACTGATACC | TGCCATCTAC | 360 |
| CTCCTGGTGT | TTGTAGTTGG | TGTCCCGGCC | AATGCTGTGA | CCCTGTGGAT | GCTTTTCTTC | 420 |
| AGGACCAGAT | CCATCTGTAC | CACTGTATTC | TACACCAACC | TGGCCATTGC | AGATTTTCTT | 480 |
| TTTTGTGTTA | CATTGCCCTT | TAAGATAGCT | TATCATCTCA | ATGGGAACAA | CTGGGTATTT | 540 |
| GGAGAGGTCC | TGTGCCGGGC | CACCACAGTC | ATCTTCTATG | GCAACATGTA | CTGCTCCATT | 600 |
| CTGCTCCTTG | CCTGCATCAG | CATCAACCGC | TACCTGGCCA | TCGTCCATCC | TTTCACCTAC | 660 |
| CGGGGCCTGC | CCAAGCACAC | CTATGCCTTG | GTAACATGTG | GACTGGTGTG | GGCAACAGTT | 720 |
| TTCTTATATA | TGCTGCCATT | TTTCATACTG | AAGCAGGAAT | ATTATCTTGT | TCAGCCAGAC | 780 |
| ATCACCACCT | GCCATGATGT | TCACAACACT | TGCGAGTCCT | CATCTCCCTT | CCAACCTCTAT | 840 |
| TACTTCATCT | CCTTGGCATT | CTTTGGATTG | TTAATTCCAT | TTGTGCTTAT | CATCTACTGC | 900 |
| TATGCAGCCA | TCATCCGGAC | ACTTAATGCA | TACGATCATA | GATGGTTGTG | GTATGTTAAG | 960 |
| GCGAGTCTCC | TCATCCTTGT | GATTTTTFACC | ATTGCTTTTG | CTCCAAGCAA | TATTATTCTT | 1020 |
| ATTATTACAC | ATGCTAACTA | CTACTACAAC | AACACTGATG | GCTTATATTT | TATATATCTC | 1080 |
| ATAGCTTTGT | GCCTGGGTAG | TCTTAATAGT | TGCTTAGATC | CATTCTTTTA | TTTTCTCATG | 1140 |
| TCAAAAACCA | GAAATCACTC | CACTGCTTAC | CTTACAAAAT | AGTGAAATGA | TCTTAGAGAA | 1200 |
| CAAGGACAGC | CATCACAGAG | AACG | | | | 1224 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| ACAGGCATGG | AAAATGATAC | AAACAACCTTG | GCAAAGCCAA | CCTTACCCAT | TAAGACCTTT | 60 |
| CGTGGAGCTC | CCCCAAATTC | TTTTGAAGAG | TTCCCCTTTT | CTGCCTTGGA | AGGCTGGACA | 120 |
| GGAGCCACGA | TTACTGTAAA | AATTAAGTGC | CCTGAAGAAA | GTGCTTCACA | TCTCCATGTG | 180 |
| AAAAATGCTA | CCATGGGGTA | CCTGACCAGC | TCCTTAAGTA | CTAAACTGAT | ACCTGCCATC | 240 |
| TACCTCCTGG | TGTTTGTAGT | TGGTGTCCCG | GCCAATGCTG | TGACCCTGTG | GATGCTTTTC | 300 |
| TTCAGGACCA | GATCCATCTG | TACCACTGTA | TTCTACACCA | ACCTGGCCAT | TGCAGATTTT | 360 |
| CTTTTTTGTG | TTACATTGCC | CTTTAAGATA | GCTTATCATC | TCAATGGGAA | CAACTGGGTA | 420 |
| TTTGGAGAGG | TCCTGTGCCG | GGCCACCACA | GTCATCTTCT | ATGGCAACAT | GTACTGCTCC | 480 |
| ATTCTGCTCC | TTGCCTGCAT | CAGCATCAAC | CGCTACCTGG | CCATCGTCCA | TCCTTTCACC | 540 |
| TACCGGGGCC | TGCCCAAGCA | CACCTATGCC | TTGGTAACAT | GTGGACTGGT | GTGGGCAACA | 600 |
| GTTTTCTTAT | ATATGCTGCC | ATTTTTTCATA | CTGAAGCAGG | AATATTATCT | TGTTTCAGCCA | 660 |
| GACATACCA | CCTGCCATGA | TGTTCAACAAC | ACTTGCGAGT | CCTCATCTCC | CTTCCAACCTC | 720 |
| TATTACTTCA | TCTCCTTGGC | ATTCTTTGGA | TTCTTAATTC | CATTTGTGCT | TATCATCTAC | 780 |
| TGCTATGCAG | CCATCATCCG | GACACTTAAT | GCATACGATC | ATAGATGGTT | GTGGTATGTT | 840 |
| AAGGCGAGTC | TCCTCATCCT | TGTGATTTTT | ACCATTTGCT | TTGCTCCAAG | CAATATTATT | 900 |
| CTTATTATTC | ACCATGCTAA | CTACTACTAC | AACAACACTG | ATGGCTTATA | TTTTATATAT | 960 |
| CTCATAGCTT | TGTGCCTGGG | TAGTCTTAAT | AGTTGCTTAG | ATCCATTCTC | TTATTTTCTC | 1020 |
| ATGTCAAAAA | CCAGAAATCA | CTCCACTGCT | TACCTTACAA | AATAGTGAAA | TGATCTTAGA | 1080 |
| GAACAAGGAC | AGCCATCACA | GA | | | | 1102 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 9, 394, 395
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Met | Ile | Leu | Gln | Ile | Ser | Xaa | Arg | Leu | Arg | Asp | Gly | Thr | Gln |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Val | Ile | Lys | Met | Lys | Ala | Leu | Ile | Phe | Ala | Ala | Ala | Gly | Leu | Leu | Leu |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Leu | Leu | Pro | Thr | Phe | Cys | Gln | Ser | Gly | Met | Glu | Asn | Asp | Thr | Asn | Asn |
| | | 35 | | | | | | 40 | | | | 45 | | | |
| Leu | Ala | Lys | Pro | Thr | Leu | Pro | Ile | Lys | Thr | Phe | Arg | Gly | Ala | Pro | Pro |
| | | 50 | | | | | | 55 | | | | 60 | | | |
| Asn | Ser | Phe | Glu | Glu | Phe | Pro | Phe | Ser | Ala | Leu | Glu | Gly | Trp | Thr | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ala | Thr | Ile | Thr | Val | Lys | Ile | Lys | Cys | Pro | Glu | Glu | Ser | Ala | Ser | His |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | His | Val | Lys | Asn | Ala | Thr | Met | Gly | Tyr | Leu | Thr | Ser | Ser | Leu | Ser |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Thr | Lys | Leu | Ile | Pro | Ala | Ile | Tyr | Leu | Leu | Val | Phe | Val | Val | Gly | Val |
| | | | 115 | | | | | 120 | | | | | | 125 | |
| Pro | Ala | Asn | Ala | Val | Thr | Leu | Trp | Met | Leu | Phe | Phe | Arg | Thr | Arg | Ser |

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|---|-----|-----|
| 130 | 135 | 140 |
| Ile Cys Thr Thr Val Phe Tyr Thr Asn Leu Ala Ile Ala Asp Phe Leu | | |
| 145 | 150 | 155 |
| Phe Cys Val Thr Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn | | 160 |
| | 165 | 170 |
| Asn Trp Val Phe Gly Glu Val Leu Cys Arg Ala Thr Thr Val Ile Phe | | 175 |
| | 180 | 185 |
| Tyr Gly Asn Met Tyr Cys Ser Ile Leu Leu Leu Ala Cys Ile Ser Ile | | 190 |
| | 195 | 200 |
| Asn Arg Tyr Leu Ala Ile Val His Pro Phe Thr Tyr Arg Gly Leu Pro | | 205 |
| 210 | 215 | 220 |
| Lys His Thr Tyr Ala Leu Val Thr Cys Gly Leu Val Trp Ala Thr Val | | |
| 225 | 230 | 235 |
| Phe Leu Tyr Met Leu Pro Phe Phe Ile Leu Lys Gln Glu Tyr Tyr Leu | | |
| | 245 | 250 |
| Val Gln Pro Asp Ile Thr Thr Cys His Asp Val His Asn Thr Cys Glu | | 255 |
| | 260 | 265 |
| Ser Ser Ser Pro Phe Gln Leu Tyr Tyr Phe Ile Ser Leu Ala Phe Phe | | 270 |
| | 275 | 280 |
| Gly Phe Leu Ile Pro Phe Val Leu Ile Ile Tyr Cys Tyr Ala Ala Ile | | 285 |
| 290 | 295 | 300 |
| Ile Arg Thr Leu Asn Ala Tyr Asp His Arg Trp Leu Trp Tyr Val Lys | | |
| 305 | 310 | 315 |
| Ala Ser Leu Leu Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Ser | | |
| | 325 | 330 |
| Asn Ile Ile Leu Ile Ile His His Ala Asn Tyr Tyr Tyr Asn Asn Thr | | 335 |
| | 340 | 345 |
| Asp Gly Leu Tyr Phe Ile Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu | | 350 |
| | 355 | 360 |
| Asn Ser Cys Leu Asp Pro Phe Leu Tyr Phe Leu Met Ser Lys Thr Arg | | 365 |
| 370 | 375 | 380 |
| Asn His Ser Thr Ala Tyr Leu Thr Lys Xaa Xaa Asn Asp Leu Arg Glu | | |
| 385 | 390 | 395 |
| Gln Gly Gln Pro Ser Gln Arg Thr | | 400 |
| | 405 | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| |
|---|
| Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys |
| 1 5 10 15 |
| Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys |
| 20 25 30 |
| Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro |
| 35 40 45 |
| Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser |
| 50 55 60 |
| Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gln | Lys | Gln | Leu | Pro | Ala | Phe | Ile | Ser | Glu | Asp | Ala | Ser | Gly | Tyr | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Ser | Ser | Trp | Leu | Thr | Leu | Phe | Val | Pro | Ser | Val | Tyr | Thr | Gly | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Val | Val | Ser | Leu | Pro | Leu | Asn | Ile | Met | Ala | Ile | Val | Val | Phe | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Lys | Met | Lys | Val | Lys | Lys | Pro | Ala | Val | Val | Tyr | Met | Leu | His | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Thr | Ala | Asp | Val | Leu | Phe | Val | Ser | Val | Leu | Pro | Phe | Lys | Ile | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Tyr | Tyr | Phe | Ser | Gly | Ser | Asp | Trp | Gln | Phe | Gly | Ser | Glu | Leu | Cys | Arg |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Phe | Val | Thr | Ala | Ala | Phe | Tyr | Cys | Asn | Met | Tyr | Ala | Ser | Ile | Leu | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Met | Thr | Val | Ile | Ser | Ile | Asp | Arg | Phe | Leu | Ala | Val | Val | Tyr | Pro | Met |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Gln | Ser | Leu | Ser | Trp | Arg | Thr | Leu | Gly | Arg | Ala | Ser | Phe | Thr | Cys | Leu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Ile | Trp | Ala | Leu | Ala | Ile | Ala | Gly | Val | Val | Pro | Leu | Val | Leu | Lys |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Glu | Gln | Thr | Ile | Gln | Val | Pro | Gly | Leu | Asn | Ile | Thr | Thr | Cys | His | Asp |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Val | Leu | Asn | Glu | Thr | Leu | Leu | Glu | Gly | Tyr | Tyr | Ala | Tyr | Tyr | Phe | Ser |
| | | 260 | | | | | 265 | | | | | 270 | | | |
| Ala | Phe | Ser | Ala | Val | Phe | Phe | Phe | Val | Pro | Leu | Ile | Ile | Ser | Thr | Val |
| | 275 | | | | | 280 | | | | | 285 | | | | |
| Cys | Tyr | Val | Ser | Ile | Ile | Arg | Cys | Leu | Ser | Ser | Ser | Ala | Val | Ala | Asn |
| | 290 | | | | | 295 | | | | 300 | | | | | |
| Arg | Ser | Lys | Lys | Ser | Arg | Ala | Leu | Phe | Leu | Ser | Ala | Ala | Val | Phe | Cys |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ile | Phe | Ile | Ile | Cys | Phe | Gly | Pro | Thr | Asn | Val | Leu | Leu | Ile | Ala | His |
| | | | 325 | | | | | | 330 | | | | 335 | | |
| Tyr | Ser | Phe | Leu | Ser | His | Thr | Ser | Thr | Thr | Glu | Ala | Ala | Tyr | Phe | Ala |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Tyr | Leu | Leu | Cys | Val | Cys | Val | Ser | Ser | Ile | Ser | Ser | Cys | Ile | Asp | Pro |
| | 355 | | | | | 360 | | | | | 365 | | | | |
| Leu | Ile | Tyr | Tyr | Tyr | Ala | Ser | Ser | Glu | Cys | Gln | Arg | Tyr | Val | Tyr | Ser |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ile | Leu | Cys | Cys | Lys | Glu | Ser | Ser | Asp | Pro | Ser | Ser | Tyr | Asn | Ser | Ser |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Gly | Gln | Leu | Met | Ala | Ser | Lys | Met | Asp | Thr | Cys | Ser | Ser | Asn | Leu | Asn |
| | | | 405 | | | | | | 410 | | | | | 415 | |
| Asn | Ser | Ile | Tyr | Lys | Lys | Leu | Leu | Thr | | | | | | | |
| | | | 420 | | | | | 425 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Pro | Ser | Ala | Ala | Trp | Leu | Leu | Gly | Ala | Ala | Ile | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Ala | Ser | Leu | Ser | Cys | Ser | Gly | Thr | Ile | Gln | Gly | Thr | Asn | Arg | Ser |
| | | 20 | | | | | 25 | | | | | | 30 | | |
| Ser | Lys | Gly | Arg | Ser | Leu | Ile | Gly | Lys | Val | Asp | Gly | Thr | Ser | His | Val |
| | 35 | | | | | | 40 | | | | | 45 | | | |
| Thr | Gly | Lys | Gly | Val | Thr | Val | Glu | Thr | Val | Phe | Ser | Val | Asp | Glu | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Ala | Ser | Val | Leu | Thr | Gly | Lys | Leu | Thr | Thr | Val | Phe | Leu | Pro | Ile |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Val | Tyr | Thr | Ile | Val | Phe | Val | Val | Gly | Leu | Pro | Ser | Asn | Gly | Met | Ala |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Leu | Trp | Val | Phe | Leu | Phe | Arg | Thr | Lys | Lys | Lys | His | Pro | Ala | Val | Ile |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Tyr | Met | Ala | Asn | Leu | Ala | Leu | Ala | Asp | Leu | Leu | Ser | Val | Ile | Trp | Phe |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| Pro | Leu | Lys | Ile | Ala | Tyr | His | Ile | His | Gly | Asn | Asn | Trp | Ile | Tyr | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Glu | Ala | Leu | Cys | Asn | Val | Leu | Ile | Gly | Phe | Phe | Tyr | Gly | Asn | Met | Tyr |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Cys | Ser | Ile | Leu | Phe | Met | Thr | Cys | Leu | Ser | Val | Gln | Arg | Tyr | Trp | Val |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Ile | Val | Asn | Pro | Met | Gly | His | Ser | Arg | Lys | Lys | Ala | Asn | Ile | Ala | Ile |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Gly | Ile | Ser | Leu | Ala | Ile | Trp | Leu | Leu | Ile | Leu | Leu | Val | Thr | Ile | Pro |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Leu | Tyr | Val | Val | Lys | Gln | Thr | Ile | Phe | Ile | Pro | Ala | Leu | Asn | Ile | Thr |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Thr | Cys | His | Asp | Val | Leu | Pro | Glu | Gln | Leu | Leu | Val | Gly | Asp | Pro | Phe |
| 225 | | | | 230 | | | | | | 235 | | | | | 240 |
| Leu | Ser | Leu | Ala | Ile | Gly | Val | Phe | Leu | Phe | Pro | Ala | Phe | Leu | Thr | Ala |
| | | | 245 | | | | | 250 | | | | | | 255 | |
| Ser | Ala | Tyr | Val | Leu | Met | Ile | Arg | Met | Leu | Arg | Ser | Ser | Ala | Met | Asp |
| | | 260 | | | | | 265 | | | | | | 270 | | |
| Glu | Asn | Ser | Glu | Lys | Lys | Arg | Lys | Arg | Ala | Ile | Lys | Leu | Ile | Val | Thr |
| | 275 | | | | | 280 | | | | | 285 | | | | |
| Val | Leu | Ala | Met | Tyr | Leu | Ile | Cys | Phe | Thr | Pro | Ser | Asn | Leu | Leu | Leu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Val | Val | His | Tyr | Phe | Leu | Ile | Lys | Ser | Gln | Gly | Gln | Ser | His | Val | Tyr |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ala | Leu | Tyr | Ile | Val | Ala | Leu | Cys | Leu | Ser | Thr | Leu | Asn | Ser | Cys | Ile |
| | | | 325 | | | | | 330 | | | | | | 335 | |
| Asp | Pro | Phe | Val | Tyr | Tyr | Phe | Val | Ser | His | Asp | Phe | Arg | Asp | His | Ala |
| | | 340 | | | | | 345 | | | | | | 350 | | |
| Lys | Asn | Ala | Leu | Leu | Cys | Arg | Ser | Val | Arg | Thr | Val | Lys | Gln | Met | Gln |
| | 355 | | | | | 360 | | | | | 365 | | | | |
| Val | Ser | Leu | Thr | Ser | Lys | Lys | His | Ser | Arg | Lys | Ser | Ser | Ser | Tyr | Ser |
| | 370 | | | | 375 | | | | | | 380 | | | | |
| Ser | Ser | Ser | Thr | Thr | Val | Lys | Thr | Ser | Tyr | | | | | | |
| 385 | | | | | 390 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...29
- (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24

- (A) NAME/KEY: Other
- (B) LOCATION: 22...27
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...21
- (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: N=A or C or G or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1 5 10 15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
20 25 30
Lys Asp Asp Asp Asp Val Glu
35

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Glu Glu Phe Pro
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Thr Pro Lys

1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Arg Gly Ala Pro

1

5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu

1

5

10

15

Phe Pro Phe Ser Ala Leu Glu

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Leu Pro Ile Lys Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
 1             5             10             15
Phe Pro Phe Ser Ala Leu Glu
                20

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Leu Pro Ile Xaa Thr Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu
 1             5             10             15
Glu Phe Pro Phe Ser Ala Leu Glu
                20

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe
 1             5             10             15
Pro Phe Ser Ala Leu Glu
                20

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys

1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5